

IN THE SPECIFICATION:

Page 33, beginning at line 12, please amend the paragraph to read as follows:

Figure 10 is a representation of the N-terminal amino acid sequence of murine NR4 (SEQ ID NOS: 10 and 11).

Page 37, beginning at line 3, please amend the paragraph to read as follows:

A library was constructed λZAP II using ApoI digested genomic DNA from embryonal stem cells and screened with a pool of 32 P-labelled oligonucleotides encoding the amino acid sequence Trp-Ser-Asp-Trp-Ser (SEQ ID NO: 12) found in many members of the haemopoietin receptor family. One hybridising bacteriophage clone was found to contain a sequence that appeared to encode part of a novel member of the haemopoietin receptor family. This receptor was given the operational name NR4. The sequence of the genomic clone was used to isolate cDNAs encoding NR4 from WEHI-3B cell, peritoneal macrophage, bone marrow, skin and kidney libraries. A composite of the nucleotide sequence ({SEQ ID NO: 1}) and predicted amino acid sequence ({SEQ ID NO: 2}) of these cDNAs is shown in Figure 1. The NR4 cDNA is predicted to encode for a protein of 424 amino acid residues, containing a putative signal sequence and transmembrane domain. The extracellular region of the protein contained an immunoglobulin-like domain (amino acids 27-117), in addition to a typical haemopoietin receptor domain (amino acids 118-340) which includes four conserved cysteine residues and the characteristic Trp-Ser-Asp-Trp-Ser motif (Figure; in bold as WSXWS). The cytoplasmic tail of the new receptor was 60 amino acids in length.